



Petitioner's Docket No. MPI00-212CP1CN1M

**PATENT**

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re application of:	Coyle, Anthony J. et al.		
Application No.:	10/644,671	Group No.:	1644
Filed:	August 20, 2003	Examiner:	Ouspenski, Ilia I.
For:	SCREENING METHODS USING B7-H2 MOLECULES, MEMBERS OF THE B7 FAMILY (as amended)		

Mail Stop Amendment  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

**AMENDMENT AND RESPONSE**

Sir: In response to the Office action mailed June 21, 2006, entry and consideration of the following remarks and amendments is requested:

**Amendments to the Specification** begin on page 2 of this paper.

**Amendments to the Claims** are reflected in the listing of claims which begins on page 3 of this paper.

**Remarks/Arguments** begin on page 5 of this paper.

---

**CERTIFICATION UNDER 37 C.F.R. SECTIONS 1.8(a) and 1.10\***

I hereby certify that, on the date shown below, this correspondence is being:

**MAILING**

- deposited with the United States Postal Service in an envelope addressed to the Mail Stop Amendment, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.  
**37 C.F.R. SECTION 1.8(a)**

**37 C.F.R. SECTION 1.10\***

- with sufficient postage as first class mail.  as "Express Mail Post Office to Addressee"  
Mailing Label No.

**TRANSMISSION**

- transmitted by facsimile to the Patent and Trademark Office – 571 273 8300.

  
Signature

Sean Hunziker

(type or print name of person certifying)

Date: December 14, 2006

\*WARNING: Each paper or fee filed by "Express Mail" must have the number of the "Express Mail" mailing label placed thereon prior to mailing. 37 C.F.R. section 1.10(b). "Since the filing of correspondence under section 1.10 without the Express Mail mailing label thereon is an oversight that can be avoided by the exercise of reasonable care, requests for waiver of this requirement will not be granted on petition." Notice of Oct. 24, 1996, 60 Fed. Reg. 56,439, at 56,442.

## IN THE SPECIFICATION:

At page 1 of the specification, please amend the title as follows:

**SCREENING METHODS USING B7-H2 MOLECULES, NOVEL MEMBERS OF THE B7**  
**FAMILY**  
**AND USES THEREOF**

At pages 24-25 of the specification, please amend the paragraph beginning at page 24, line 12, as follows:

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, nonlimiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul *et al.* (1990) *J. Mol. Biol.* 215:403. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to B7-like nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to B7-like protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389. Alternatively, PSI-Blast can be used to perform an iterated search that detects distant relationships between molecules. See Altschul *et al.* (1997) *supra*. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov). Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0), which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

At page 97 of the specification, please amend the title of the abstract as follows:

**SCREENING METHODS USING B7-H2 MOLECULES, NOVEL MEMBERS OF THE B7**  
**FAMILY**  
**AND USES THEREOF**